amino-acid residue (in a polypeptide)

When two or more amino acids combine to form a *peptide*, the elements of water are removed, and what remains of each amino acid is called an amino-acid residue. α-Amino-acid residues are therefore structures that lack a hydrogen atom of the amino group (–NH–CHR–COOH), or the hydroxyl moiety of the carboxyl group (NH$_2$–CHR–CO–), or both (–NH–CHR–CO–); all units of a peptide chain are therefore amino-acid residues. (Residues of amino acids that contain two amino groups or two carboxyl groups may be joined by *isopeptide bonds*, and so may not have the formulas shown.)

The residue in a peptide that has an amino group that is free, or at least not acylated by another amino-acid residue (it may, for example, be acylated or formylated), is called N-terminal; it is at the N-terminus. The residue that has a free carboxyl group, or at least does not acylate another amino-acid residue, (it may, for example, acylate ammonia to give –NH–CHR–CO–NH$_2$), is called C-terminal.

W.B. 48

IUPAC Compendium of Chemical Terminology   2nd Edition (1997)